

Run on:		March 17, 2001, 21:52:24 ; Search time 71.96 Seconds		
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OM protein - protein search, using sw model		259.843 Million cell updates/sec		
Title:	US-09-456-306-2			
Perfect score:	2985			
Sequence:	1 MAHSYEQIDTLEAQVKKR..... GQVGAMIDLARNSNIRNIPTP 579			
Scoring table:	BLOSUM2			
Searched:	88757 seqs, 32294092 residues			
Total number of hits satisfying chosen parameters:	88757			
Maximum DB seq length:	0			
Maximum DB seq length:	200000000			
Post-processing:	Minimum Match 0%			
Database :	Maximum Match 100% Listing first 45 summaries			
SwissProt: 39; *				
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
SUMMARIES				
Result No.	Score	Query	%	
		Length	DB ID	
			Description	
1	1317.5	44.1	572	1 POXB_ECOLI
2	902.5	30.2	396	1 YI42_PSEAY
3	585.5	19.6	591	1 ILVB_METJA
4	545.6	18.8	603	1 POXB_LACPL
5	544.6	18.6	573	1 ILVB_GUTTH
6	533.5	17.9	575	1 ILVB_PORPU
7	533.5	17.9	590	1 ILVB_MCYTO
8	526	17.6	618	1 ILVB_ECOLI
9	523.5	17.5	562	1 ILVB_SPIPL
10	517.5	17.3	579	1 ILVB_ECOLI
11	507	17.0	548	1 ILVB_MCYCLE
12	503	16.9	625	1 ILVB_ARATH
13	493	16.5	670	1 POXB_STRPN
14	492	16.5	591	1 ILVI_BRANA
15	480	16.1	655	1 ILV3_BRANA
16	477	16.0	652	1 ILVB_WCAV
17	464.5	16.0	621	1 ILVB_CORG1
18	461	15.4	626	1 ILV2_TOBAC
19	454	15.2	664	1 ILV1_TOBAC
20	454	15.0	677	1 ILV1_TOBAC
21	449	15.0	575	1 ILVB_LACLA
22	441.5	14.8	637	1 ILV2_BRANA
23	422	14.1	559	1 ILVB_KLETE
24	420	14.1	574	1 ILVI_ECOLI
25	418.5	14.0	669	1 ILVB_SCOPH
26	414	13.9	687	1 ILVB_YEAST
27	393	13.2	559	1 ILVB_KLEPN
28	390.5	13.1	573	1 ILVI_HAEIN
29	385.5	12.9	571	1 ILVI_BUCAP
30	356	11.9	592	1 GCL_ECOLI
31	332	11.1	494	1 Y663_METJA
32	316.5	10.6	540	1 ILVX_BDCSU
33	313	10.5	547	1 O50613_mycobacteri

RA Recny M.A.; Grabau C.; Cronan J.E.JR.; Hager L.P.;
 RT Characterization of the alpha-peptide released upon protease
 activation of pyruvate oxidase.
 RT J. Biol. Chem. 260:14287-14291(1985).
 RN [6]
 SEQUENCE OF 1-22 FROM N A.
 RX MEDLINE=4293172; PubMed=8022274;
 RA Chang Y.Y.; Wang A.Y.; Cronan J.E. JR.;
 RT *Experiments with *Escherichia coli* pyruvate oxidase (POXB) depends on
 the sigma factor encoded by the rpoS(katF) gene.
 RL Mol. Microbiol. 11:1019-1028(1994).
 -I- CATALYTIC ACTIVITY: PYROVATE + FERRICYTOCHROME B1 + H(2)O = CO(2)
 + ACETATE + FERROCYTOCHROME B1.
 -I- COFACTOR: THIAMINE PYROPHOSPHATE, FAD AND MAGNESIUM ION.
 -I- SUBUNIT: HOMOTETRAMER.
 -I- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED.
 -I- PRODUCES A PEPTIDE (ALPHA-PEPTIDE) AND MIMICS THE ACTIVATION OF
 ENZYME BY PHOSPHOLIPIDS. THE PROTEOLYTIC CLEAVAGE ALSO RESULTS IN
 THE LOSS OF THE HIGH AFFINITY LIPID-BINDING SITE OF THE ENZYME.
 -I- SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.
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 or send an email to licensee@isb-sib.ch).
 CC
 DR AE00018; AAC73958.1; --.
 DR D90724; BA35585.1; --.
 DR EMBL S73368; AAB31180.1; --.
 DR EMBL M28208; AAB59101.1; --.
 DR EMBL L47888; AAB59102.1; --.
 DR EMBL L47889; AAB59103.1; --.
 DR EMBL L47890; AAB59104.1; --.
 DR EMBL L47891; AAB59105.1; --.
 DR EMBL L47892; AAB59106.1; --.
 DR EMBL L47893; AAB59107.1; --.
 DR EMBL L47894; AAB59108.1; --.
 DR EMBL L47895; AAB59109.1; --.
 DR PIR; R23648; DEBPC.
 DR HSSP; P37003; IPW.
 DR SWISS-2DPAGE; P07003; COLI.
 DR ECO2DBASE; G058_0; 6TH EDITION.
 DR ECOGENE; EG10754; POXB.
 DR INTERPRO; IPR003199; --.
 DR PFAM; PF00205; TPP_enzymes; 1.
 DR PROSITE; PS00187; TPP_ENZYMES; 1.
 KW Oxidoreductase; Flavoprotein; FAD; Thiamine pyrophosphate; Magnesium;
 KW Membrane; Lipid binding.
 FT PEPTRIDE 550 572
 FT ACT_SITE 50 50
 FT PEPTRIDE 550 572
 FT ALPHA-PEPTIDE.
 FT BY SIMILARITY.
 FT A->T; IN POXB1.
 FT A->V; IN POXB4.
 FT D->P; IN POXB15; NORMAL ACTIVITY.
 FT E->P; IN POXB; LOSS OF ACTIVITY.
 FT R->G; IN POXB10; REDUCED ACTIVITY; MAY
 FT INTERACT LESS WITH MEMBRANES.
 FT MISSING; IN POXB5.
 FT MISSING; IN POXB7.
 FT MUTAGEN 564 572
 FT MUTAGEN 570 572
 FT MUTAGEN 560 560
 FT MUTAGEN 564 564
 FT MUTAGEN 572 572
 FT MUTAGEN 549 572
 FT MUTAGEN 564 572
 FT MUTAGEN 570 572
 FT MUTAGEN 364 365
 FT CONFLICT 364 365
 FT CONFLICT 414 416
 SQ SEQUENCE 572 AA; 62011 MW; 57B3BB9E3A92BDBA CRC64;

Query Match 30.2%; Score 902.5; DB 1; Length 396;
 Best Local Similarity 49.0%; Pred. No. 3.6e-52; Gaps 4;
 Matches 176; Conservative 72; Mismatches 98; Indels 13;

Oy 6 ABQOLIDTLEAQGKRYGLVGDSDLNPVDAY-RQSDEWVIRNEEAFAAGAEELTG 64
 Db 7 ADVTEILHLVACKVRYGVVGDSLNGLTDLRRGGDIDWHRHESSAFAHGAEEHTG 66

Oy 65 ELAVCAASCGPGNTHLIGQLYDSDRNGAKVLA1ASHPSADIGSTFQETPELKECS 124
 Db 67 ELAVCAGSCPGPNHLINGLFDCBRSRVPLAAHIPSADIGSTFQETPELKECS 126

Oy 125 GCEWMNGEGERILHHAQSTMAGKGVSVVVIQDIAKEDAGDGTYSNSTISGTPVV 184
 Db 127 HYCELVSSPGLCPVLESRAAVGLRGVAVVILIPDQVALRESNAKPAAGASMALRPPV 186

Oy 185 FPDTEPENALVEATNAKSVTLFCAGVKNRARQVLEAERIKSPGHAGKGQYQHEN 244
 Db 187 OPAADVDAQOLLNDNSGKVFLLCGRCAGAHDPKLKAERALKAPIVHARGGKKEYDN 246

Oy 245 PFEVGMSGLIGYGCYACVADASNEADDLILLGTOPPYSPDLPKD-NVAQDINGAHIGRTV 303
 Db 247 PYDVGWMTGLIGRSGYHAMLNCDTMLMGTOPPYFQYPADAKIQAQDVPRLENGRRL 306

Oy 304 KYPVTGDAVATIENTLPHVKEKTDRLMRKLAHERK-----LSVWETVTHN 352
 Db 307 DLMGVDSATIGAILPKLKARTDRAYLDACL-AHYRKAREGCLDELPSPASDASPETHN 364

RESULT 3

ID ILVB_METJA STANDARD; PRT; 591 AA.

AC 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE PROBABLE ACETOYLACETATE SYNTHASE LARGE SUBUNIT (EC 4.1.3.18) (AHAS)
 DE (ACETOHYDROXY-ACID SYNTHASE LARGE SUBUNIT) (ALS).
 GN ILVB OR MJ0277.

OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
 OC Methanococcus.
 RN [1]

SEQUENCE FROM N.A.

RP STRAIN="JAL-1" / DSM 2661 / ATCC 43067;

RC MEDLINE=96337999; PubMed=8688087;

RX Built C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 Kerlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,
 Overbeck R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
 Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 Blenk H.-P., Frasier C.M., Smith H.O., Weese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
 jannaschii.";
 RL 273:1058-1073(1996).

CC -1- CATALYTIC ACTIVITY: 2-ACETOYLACETATE + CO(2) = 2-PYRUVATE.
 CC -1- COFACTOR: THIAMINE PYROPHOSPHATE, AND MAGNESIUM ION (BY
 CC SIMILARITY);
 CC -1- PATHWAY: FIRST STEP IN VALINE AND ISOLEUCINE BIOSYNTHESIS.
 CC -1- SUBUNIT: DIMER OF LARGE AND SMALL CHAINS (BY SIMILARITY).
 CC -1- SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.

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CC DR EMBL; U67483; AAB98265.1; -.

CC DR HSPP; P06169; IYPD.

CC DR TIGR; MJ0277; -.

CC DR INTERPRO; IPR000399; -.

CC DR PFAM; PF00205; TPP_enzymes; 1.

CC DR PROSITE; PS00187; TPP_ENZYMES; 1.

CC KW Branched-chain amino acid biosynthesis; Flavoprotein; Magnesium; Thiamine pyrophosphate; Lyase.

CC FT ACT SITE 47 47 BY SIMILARITY.

CC SQ 591 AA; 64492 MW; DB398C926D9B3A9D CRC64;

Query Match 19.6%; Score 586.5; DB 1; Length 591;
 Best Local Similarity 29.5%; Pred. No. 3.2e-31; Gaps 16;
 Matches 166; Conservative 109; Mismatches 247; Indels 41;

Oy 6 ABQOLIDTLEAQGKRYGLVGDSDLNPVTDVAVROSDIERVMVRNEEAFAANGESLITGE 65
 Db 4 AEAIKALEAEQVSKIFGPGAMLPYDALIDSVLWHLTRHEQAMHNGFARKSGE 63

Oy 66 LAVCAASCGPGNTHLIGQLYDSDRNGAKVLA1ASHPSADIGSTFQETPELKECS 125
 Db 64 AGIVCVSISPGAMNLVNGIATWADSPSERVIALTQVETPKLGNDAEQIDALGLFEMIT 123

Oy 126 YCEWMNGEGERILHHAQSTMAGKGVSVVVIQDIAKEDAGDGTYSNSTISGTPVV 184
 Db 124 HMFQIKRPEETETFRAAFELATTCGPGVPHIDLKPVQDGIDIEYPPIPQVLDGYK 183

Oy 182 PYVFPDTEAALVEATNAKSVTLFCAGGV--KNARQVLLAEEKTSPIGHALGKQY 239
 Db 184 PKTVGHPQLQKKAALKIASESERPVILLAGGVVISGASEELLRLAEFVPRVPTTLMKGKC 243

Oy 240 IQHENPPEVGMSGLIGYGCYACVADASNEADDLILLGTOPPYSD-----FLPKDVAQD 291

Db 244 FREDHPFLAGMIGMHGKKAANVATEDVCDLVAIAGCRE--SDRVTDGDIYFAPAEKIH 301

Oy 292 INCAHIGRTTVKYPVIGDAVATIENILP---HKEKTDRSFLDRMLKAIERKLSVV 346
 Db 302 LDPAEGLKVNRAIDIPIVGDAKVNLRLIAALIALEIKDK--ETWLBIYIEL--KKLSPM 357

Oy 347 ETYTHNVEKHPVTPHEY--VASTINELAD--KDAVFTVDTGMCNWHRARYTENPEGTR 400
 Db 358 MFDDK---PIKPQRFVKDLMEVNLNEIDSKLNKNTITTDVGQNQWMWMMFKT-KMPR 411

Oy 401 DEVGSFRHGTMANALPAIAGAQSVDRRQVAMCGDGGGLGMIGELITVLUHOLPUKAV 460
 Db 412 SFLASGGLGTMQFGFPRKAIGVAKPVANVVISITDQGFLMNSQELATISEDIPVVICI 471

Oy 461 FNNSLGMV-KLEMVLEGQPERGTD-HEEVNFIAAAGKSVRTPKKVREOLEAN 518
 Db 472 FDNRITLGWVQWONLYVGORQSEVHUGLSEPDVPLAKBSYGVKADRITSPEIKEKLI 531

Oy 519 AVPGPVLLIDVTDP-NAL-SIPP 539
 Db 532 LSNEPYLVIDIVDPAEALPMVPP 554

RESULT 4

ID POXB_LACP1 STANDARD; PRT; 603 AA.

AC 23763;

DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)

DE PYRUVATE OXIDASE (EC 1.2.3.3) (PYRUVIC OXIDASE) (POX).

CC OS Lactobacillus plantarum.

CC OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;

CC OC Lactobacillus.

CC RN [1]

CC RP X-RAY CRYSTALLOGRAPHY (2.5 AND 2.1 ANGSTROMS) OF WILD-TYPE AND MUTANT.

CC RX MEDLINE=94194507; PubMed=14524;

RA Muller Y.A., Schumacher G., Rudolph R., Schulz G.E.;

"The refined structures of a stabilized mutant and of wild-type pyruvate oxidase from *Lactobacillus plantarum*."; J. Mol. Biol. 237:315-335(1994).
 X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
 MULLER Y.A., Schulz G.E.; Müller Y.A., Schulz G.E.;
 "Structure of the thiamine- and flavin-dependent enzyme pyruvate oxidase.";
 Science 259: 965-967(1993).
 -!- FUNCTION: IMPORTANT FOR THE AEROBIC GROWTH. DECARBOXYLATES PYRUVATE IN FOUR STEPS. THE ENERGY RELEASED IS PARTIALLY STORED IN ACETYL PHOSPHATE.
 -!- CATALYTIC ACTIVITY: PYRUVATE + ORTHOPHOSPHATE + O(2) + H(2)O = ACETYL PHOSPHATE + CO(2) + H(2)O.
 -!- COFACTOR: THIAMINE PYROPHOSPHATE, FAD AND MAGNESIUM ION.
 -!- SUBUNIT: HOMOTETRAMER.
 -!- DOMAIN: EACH MONOMER IS DIVIDED INTO THREE DOMAINS, EACH OF WHICH CONTAINS A SIX-STRAINED PARALLEL BETA SHEET SURROUNDED BY ALPHA HELICES.
 CC PROSTH; PS00187; TPP_ENZIMES; 1.
 DR OXIDOREDUCTASE; Flavoprotein; FAD; Thiamine pyrophosphate; Magnesium;
 KW 3D structure.
 FT DOMAIN 1 191 CORE.
 FT DOMAIN 192 FAD.
 FT DOMAIN 343 TPP.
 FT ACT_SITE 59 BY SIMILARITY.
 FT METAL 447 MAGNESIUM.
 FT METAL 474 MAGNESIUM.
 FT METAL 476 MAGNESIUM.
 FT STRAND 10 12
 FT HELIX 13 23
 FT TURN 24 25
 FT STRAND 28 31
 FT HELIX 35 46
 FT TURN 47 50
 FT STRAND 52 55
 FT HELIX 59 73
 FT STRAND 77 81
 FT TURN 83 84
 FT HELIX 85 88
 FT TURN 89 90
 FT HELIX 91 99
 FT TURN 100 101
 FT STRAND 104 110
 FT TURN 113 117
 FT TURN 121 122
 FT HELIX 127 130
 FT TURN 131 133
 FT STRAND 136 139
 FT TURN 144 145
 FT HELIX 146 160
 FT TURN 161 161
 FT STRAND 163 169
 FT TURN 170 171
 FT STRAND 172 174
 FT TURN 176 178
 FT HELIX 179 180
 FT TURN 186 188
 FT STRAND 186 196
 FT HELIX 199 211
 FT STRAND 215 219
 FT HELIX 221 237
 FT TURN 238 238
 FT STRAND 241 243
 FT HELIX 245 247
 FT TURN 249 254
 CC PFM; PF00205; TPP_enzymes; 1.
 DR PROSTH; PS00187; TPP_ENZIMES; 1.
 DR 1POW; 31-JAN-94.
 PDB; 1POX; 31-JAN-94.
 INTERPRO: IPR000399; -.

FT	TURN	256	257
FT	STRAND	258	258
FT	HELIX	268	276
FT	STRAND	279	283
FT	TURN	288	298
FT	STRAND	301	306
FT	HELIX	309	311
FT	TURN	312	313
FT	STRAND	320	323
FT	HELIX	326	336
FT	TURN	336	387
FT	STRAND	389	392
FT	HELIX	396	404
FT	TURN	409	410
FT	STRAND	412	414
FT	TURN	422	423
FT	STRAND	468	473
FT	HELIX	476	476
FT	TURN	478	487
FT	STRAND	491	496
FT	HELIX	495	509
FT	TURN	510	510
FT	STRAND	512	516
FT	STRAND	518	518
FT	HELIX	519	532
FT	TURN	533	535
FT	STRAND	538	543
FT	TURN	552	553
FT	TURN	559	561
FT	HELIX	564	574
FT	TURN	575	575
FT	TURN	577	578
FT	HELIX	582	588
FT	TURN	589	590
SQ	SEQUENCE	603 AA;	66141 MW;
Query Match 18.8%; Score 560; DB 1; Length 603;			
Best Local Similarity 27.5%; Pred. No. 1.8e-29; Matches 147; Conservative 116; Mismatches 251; Indels 20; Gaps 8;			
Qy	9	LIDTLEAQGKRIYGIVGQDSINPVDAV-RQSDETWVHRNEAAFFAGAESLTIGEL	66
Db	17	VIKVLEAWGVPHLYGIPGGGSINSMDALSAERDRHYIQVREEVGAMAAAADAKLTGKL	76
Qy	67	AVCAASCGPANTHLIOTGLYSRHSNRKAVALIAASHIPSQAQGSTFOETHEBELLRECSY	126
Db	77	GVCFGSAGPGSTHLMNGLYDAREDKHVPVLIALIGQRTGTTGNMNTFOEMMENPIKADV	136
Qy	127	CEMVNQEGERILHAIQSMAGKGVSVVWPGIAKEADGDPYNSNISCPVW	185
Db	137	NVTAVNAATLPHVIDAIRRAYAHOGVAVVQIPVLPWQOQPAEDWYASNSYQPLPE	196
Qy	186	FEVGMGLLGAGCYDASNEADLILGTPYSD--FLPKDVAQDINGAHIGR	301
Db	257	PDPTEAALVAFAINAKSVTFCGAGVKNARAQVLEAEKKSPGHALGKQYIHEP	245
Qy	302	TVKPYTGDAVATENILPVKEKTDSEFDRLM--KAERKISSVWEPYTHVEKHP	358
Db	317	KTDIAVLADAOKTAAILAQVSERESTPWWQANLANVKNRVLASLED-----KQEGP	370

QY	359	IIEPVVAVSINELADKDAVFTVDTGMCNNWHRHARVYIENPGEFGTFRGTMANALPHA	418	
CC	or send an email to license@lsb-sib.ch.			
Db	371	LQAVQVILRAVANKIAEPAIDAYTSDVGDINNANRHLKLTPSNRHITSNL-FATMGVGTPGA	429	
DR	EMBL; Z75208; CAA9561.1; -			
DR	M87009; AAB2250.1; -			
DR	EMBL; Z99118; CAB4791.1; -			
DR	SUBLIST; BG10670; ILVB.			
DR	INTERPRO; IPR00339; -			
DR	PFAM; PRO0205; TPP_enzymes; 1;			
DR	PROSITE; PS00187; TPP_ENYMES; FALSE_NGC			
DR	ACETOLACTATE SYNTHASE LARGE SUBUNIT (EC 4.1.3.18) (AHAS)			
DE	(ACETOHYDROXY-ACID SYNTHASE LARGE SUBUNIT) (ALS) (VEGETATIVE PROTEIN			
DE	TIVB.			
GN	OS	Bacillus subtilis.		
OC	Bacteria; Firmicutes; Bacillus/Clostridium group;			
OC	Bacillus/Staphylococcus group; Bacillus.			
RN	[1]			
SEQUENCE FROM N.A.				
RA	Vandevoort M.A., Vander Horn P.B., Rafael J.A., Grandoni J.A., Zahler S.A.; Submitted (XYY-1992) to the EMBL/GenBank/DBJ databases.			
RL	Watson A., Carter N., Brignell C.S., Guy J.B., Piper K., Sanders J., Emmerson P.T., Harwood C.R.; "the diab-pheo (256 degres-240 degrees) region of the Bacillus subtilis chromosome containing genes responsible for stress responses, the utilization of plant cell walls and primary metabolism.", Microbiology, 142:3067-3078(1996).			
RN	[2]			
SEQUENCE FROM N.A.				
RC	STRAIN=168;			
RX	MEDLINE=97124191; Pubmed=8969504;			
RA	Wipat A., Carter N., Brignell C.S., Guy J.B., Piper K., Sanders J., Emmerson P.T., Harwood C.R.; "the diab-pheo (256 degres-240 degrees) region of the Bacillus subtilis chromosome containing genes responsible for stress responses, the utilization of plant cell walls and primary metabolism.", Microbiology, 142:3067-3078(1996).			
RN	[3]			
SEQUENCE OF 1-20 FROM N.A.				
RX	MEDLINE=92250415; Pubmed=1577690;			
RA	Grandoni J.A., Zahler S.A., Calvo J.M.; "Transcriptional regulation of the liv-leu operon of Bacillus subtilis.", J. Bacteriol., 174:3212-3219(1992).			
RN	[4]			
SEQUENCE OF 1-14.				
RC	STRAIN=TS58;			
RX	MEDLINE=97443988; Pubmed=9298659;			
RA	Antelmann H., Bernhardt J., Schmid R., Mach H., Voelker U., Hockeck M.; "First steps from a two-dimensional protein index towards a response-RT regulation map for <i>Bacillus subtilis</i> .", Electrophoresis 18:1451-1463(1997).			
CC	- - CATALYTIC ACTIVITY: 2-ACETOLACTATE + CO(2) = 2-PYRUVATE (THIS ENZYME ALSO CATALYZES FORMATION OF 2-ACETO-2-HYDROXYBUTANOATE).			
CC	- - COFACTOR: THIAMINE PYROPHOSPHATE, AND MAGNESIUM ION.			
CC	- - PATHWAY: FIRST STEP IN VALINE AND ISOLEUCINE BIOSYNTHESIS.			
CC	- - SUBUNIT: DIMER OF LARGE AND SMALL CHAINS.			
CC	- - SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/).			
RESULT	5			
ILVB_BACSU	STANDARD;	PRT;	573 AA.	
ID	ILVB_GUTH	STANDARD;	PRT;	573 AA.
AC	078518;			
DT	15-DEC-1998 (Rel. 37, created)			
DT	15-DEC-1998 (Rel. 37, last sequence update)			
DR	15-TUL-1999 (Rel. 38, last annotation update)			
DE	ACETOLACTATE SYNTHASE LARGE SUBUNIT (EC 4.1.3.18) (AHAS)			
DE	(ACETOHYDROXY-ACID SYNTHASE LARGE SUBUNIT) (ALS).			
GN	ILVB			
OS	Gulliardia theta (Cryptomonas ph).			
OG	Chloroplast.			

Db	77 KVGVCFATSGPGATANVSGIATAHDSVPLAITGGVGRPEIGTDAFOEVNIFGTLPIV 136	CC modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/)
Qy	125 GYCEMWNGEGERILHHAQSTMACK-GVSVVWIRPGDIAKEDAGDGTSNSTIISGG-- 180	CC or send an email to license@isb-sib.ch).
Db	137 KHSVVVRDPROMSRTVAEAFKICKHORGPVLIDPVKDVGLE---KFNFVERGQVK 191	CC
Qy	181 ---TPVFPDPTEAALVEAINNAKSVTLCGAG--VKNARAVIELAEKIKSPIGHAL 234	DR TUBERCULIST; RV003C; -.
Db	192 IPGCRPLSLNLSKRSQQLMAKMTQSOSQPLLIGGGATISDAHSTIKELVLDYKPVVTTL 251	DR INTERPRO; IPRO0399; -.
Qy	235 GCKQYI-QHENIPFENGSCGLGGACVADASNEADLLTIGDE---PSDFLPKDVA 288	DR PROTEIN; PF00205; TPP_enzymes; 1.
Db	252 MKGKTIENEDSEFCLGMLGMIGTAYANFAVSECDLIALGARFDRTGKDEFAGNAQVI 311	DR PROTEIN; P500187; TPP_ENZMES; 1.
Qy	289 QVDINGAHAIGRTTVKVPVNGDVAAATTENILPHVKETDSFLDRMLKAHERKLSSVET 348	KW Branched-chain amino acid biosynthesis; Flavoprotein; Magnesium; Thiamine pyrophosphate; Lyase.
Db	312 HWDIDPAEVGNRNPQVAIWDVTEVUTSLNLNNKF-KPYPEQITISQER-IHRWQQ 369	FT ACT SITE 84 BY SIMILARITY.
Qy	349 YTHINV-EKHPVTPHEVAVSILNEADKDAVFTDVGMCNTWHARYTENPECTRDVGFSR 407	SQ SEQUENCE 618 AA; 6612 MW; 9E0523F4AD6EC6AF CRC64;
Db	370 YPLLVPKKSTISPOELVTTNOLA-ODAYFTPDYQHQHOMSAQFLK--VKSCHKWISSAG 426	Query Match 17.6%; Score 526; DB 1; Length 618; Best Local Similarity 29.4%; Pred. No. 3.1e-22; Matches 166; Conservative 88; Mismatches 256; Indels 54; Gaps 14;
Qy	408 HCTMANALPHAGAQSVDRNQVIAMCGDGGLGLMLGGELTYKLHOLPLKAVVNNSLG 467	Qy 6 ABQOLIDTLEAOVVKRITYGLVNGDSLNPIVAVROQ-DIEWAVWNEAAFAAGAESLITG 64
Db	427 LGTMGVGLPAMIGAQVAHPNPLVTCVSGDSSFQMNQELGTIAQKLPIKVITNNRWQG 486	Db 41 AQAVIRSKLELGVDVFGIPGAVLVRVYDPLFDSKKLRHVLRHEGAGHAAASGYAHVTC 100
Qy	468 MKVL-----EMIYRCQEPFGTDHEEVNFETAAAGIKSVRJHDPKVREOLA 515	Qy 65 ELAVCAASCGGENTHJLQGDLSHNRGAKVIAIASIIPSAGSISFTQETIPELFKECS 124
Db	487 MVRQWQAFQGERRYSHSRMTECAP-----INFOKLAEEFGKRAFTVNRRNMESSLK 537	Db 101 RYGVCMATSGPGATNLVTPALADAQMSDIPVAVTGOVGRGLGTDQFADISGTMPT 160
Qy	516 EALAYEGPVLDIVDTPNALSIPI--PTIWEQVMGFSK 551	Qy 125 GYCEMWNGEGERILHHAQSTMACK-GVSVVWIRPGDIAKEDAGDGTS--NSTIISG 180
Db	538 DAMKYPGPVLLDCQVTEMENCYPMVAPGKSNAQMIQIAK 576	Db 161 KINFLVRSGDDIPRVIAEHTIAASGRPGAVLVDIPKDYI--SOTCEWPPRMELPGV 217
RESULT 8		
ILVB_MYCTU	STANDARD; PRT; 618 AA.	Qy 181 TPVFPDPTEAALVEAINNAKSVTLCGAVKNARA-QVLELAERIKSPIGHALGGQ 238
ID 053250;		Db 218 KPNTKHSRSQVREAAKLAARKPVLYVGCGVIRGATEQRELABLTTGIPVVTLMARC 277
DT 30-MAY-2000 (Rel. 39, Last sequence update)		Qy 239 YIQHENIPFENGSCGLGGACVADASNEADLLTIGDE---PSDFLPKDVA 292
DT 30-MAY-2000 (Rel. 39, Last annotation update)		Db 278 AEPDSHQRNLGMGPMSGHGVAVAVALORSDSLJIALGTRFDRTGKLDSPAPEKVIHADI 337
DE ACETO-LACTATE SYNTHASE (EC 4.1.3.18) (ACETOHYDROXY-ACID SYNTHASE)		Qy 293 NGAHIGRRTTVKVPVNGDVAAATTENILPHVKETDSFLDRMLKAHERKLSSVVE--- 347
DE GN ILVB OR RV3003C OR MTW012.17C.		Db 338 DPAEIKRNHRADVPTGDKVAVITEI-----AMLRHH--IPTGIAEDAWN 382
OS Mycobacterium tuberculosis.		Qy 348 TYTHINV-EKHPV-----HPEVAVSILNEADKDAVFTDVGMCNTWHARYTENPE 397
OC Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.		Db 383 AYLNGVTKRTPLSYGPOSQDGSLSPESVIEKGELAGPDAFVAGYQHQHQAOFTRY-E 441
OC (1) SEQUENCE FROM N.A.		Qy 398 GTRDFVGFSFRGTMANALPHAGAQSVDRNQVIAMCGDGGLGLMLGGELTYKLHOLPLK 457
RC STRAIN-H37RV;		Db 442 KPRSWLNLSGGLGTMGAIPAAAGKALPGEVTAIWIDGDSQFQMTNOELATCNAVEGIPVK 501
RX MEDLINE=9829587; PubMed=9634230;		Qy 458 AVVENNISLGAHKV-LIMLVQEOPFCTD---HEVNFETAAAGIKSVRITDKVR 511
RA Cole S.T., Brosh R., Parkhill J., Garnier T., Churcher C., Harris D.,		Db 502 VALINNGNLAGVQRMWSLWVRSYDTHLASHRIPDFKRLAEAGCVLRCEREDVY 561
RA Gordon S.V., Elsegood K., Gas S., Barry C.E. III, Tekala F.,		Qy 512 EQLAELAYEGPVLDIVDTPNA 534
RA Badcock K., Basham D., Chillingworth T., Connor R.,		Db 562 DVINQARAINDCPWWIDFINGADA 585
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,		
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,		
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,		
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E.,		
RA Taylor K., Whitehead S., Barrell B.G.;		
RT "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.",		
RL Nature 393:537-544 (1998).		
CC -1- CATALYTIC ACTIVITY: 2-ACETOLACTATE + CO(2) = 2 PYRUVATE.		
CC -1- CATALYTIC ACTIVITY: THIAMINE PYROPHOSPHATE, AND MAGNESIUM ION (BY SIMILARITY).		
CC -1- PATHWAY: FIRST STEP IN VALINE AND ISOLEUCINE BIOSYNTHESIS.		
CC -1- SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.		
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RESULT 9		
ILVB_ECOLI	STANDARD; PRT; 562 AA.	
ID ILVB_ECOLI		
AC P08142;		
DT 01-AUG-1988 (Rel. 08, Created)		
DT 01-AUG-1988 (Rel. 08, Last sequence update)		
DT 15-DEC-1998 (Rel. 37, Last annotation update)		
DE ACETO-LACTATE SYNTHASE ISOCIME I LARGE SUBUNIT (EC 4.1.3.18) (AHAS-I)		
DE (ACETOHYDROXY-ACID SYNTHASE I LARGE SUBUNIT) (ALS-I).		
GN ILVB.		
OS Escherichia coli.		
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;		

[1]	SEQUENCE FROM N.A.
RX	RP
RA	MEDLINE=85242084; PubMed=2989782;
RA	Wek R.C., Haussler C.A., Hatfield G.W.;
RT	"The nucleotide sequence of the ilvBN operon of <i>Escherichia coli</i> : sequence homologies of the acetohydroxy acid synthase isozymes.";
RT	Nucleic Acids Res. 13:3995-4010(1985).
RN	[2]
RN	SEQUENCE FROM N.A.
RX	RP
RA	MEDLINE=85242083; PubMed=2989781;
RA	Friden P., Donegan J., Mullen J., Tsui P., Freundlich M.;
RT	"The ilvB locus of <i>Escherichia coli</i> K-12 is an operon encoding both subunits of acetohydroxyacid synthase I";
RT	Nucleic Acids Res. 13:3979-3993(1985).
RN	[3]
RN	SEQUENCE FROM N.A.
RX	RP
RA	MEDLINE=9315143; PubMed=7686882;
RA	Burland S.D., Plunkett G. III, Daniels D.L., Blattner F.R.;
RT	"DNA sequence and analysis of 136 kilobases of the <i>Escherichia coli</i> genome: organizational symmetry around the origin of replication.;"
RT	Genomics 16:553-561(1993).
CC	-I- CATALYTIC ACTIVITY: 2-ACETOLACTATE + CO(2) = 2-PYRUVATE (THIS ENZYME ALSO CATALYZES FORMATION OF 2-ACETO-2-HYDROXYBUTANOATE).
CC	-I- COFACTOR: THIAMINE PYrophosphate, AND MAGNESIUM ION.
CC	-I- PATHWAY: FIRST STEP IN VALINE AND ISOLEUCINE BIOSYNTHESIS.
CC	-I- SUBUNIT: DIMER OF LARGE AND SMALL CHAINS.
CC	-I- MISCELLANEOUS: E. COLI CONTAINS GENES FOR 3 AHAS ISOZYMES: ILVBN, ILVGM AND ILVTH.
CC	-I- SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
DR	EMBL; J01633; AAA24017.1; -.
DR	EMBL; X02541; CAA26387.1; -.
DR	EMBL; L10328; AAA62023.1; -.
DR	EMBL; AE00044; AAC76694.1; -.
DR	PIR; A23803; YC8C1L.
DR	SWISS-2DPAGE; P08142; COL1.
DR	ECO2DBASE; D057.0; 6TH EDITION.
DR	EGCogene; EG10494; ILVB.
DR	INTERPRO; IPR00399; -.
DR	PFAM; PF00205; TPP_enzymes; 1..
DR	PROSITE; PS00187; TPP_ENZYMES; 1..
KW	BRANCHED-CHAIN AMINO ACID BIOSYNTHESIS; 1..
KW	Thiamine pyrophosphate; Lyase.
FT	ACT_SITE 60 60 BY SIMILARITY.
SQ	SEQUENCE 562 AA; 60440 MW; 70F8A3128031353C CRC64;
Query	17.5% Score 523.5; DB 1; Length 562; Best Local Similarity 27.9%; Pred. No. 4e27; Matches 162; Conservative 108; Mismatches 162; Indels 71; Gaps 17; CC
QY	6 AE0LIDITLEAQGKWRIGLNGISLNPLTVDAVROS-DIEWHWRNEEAAFAAGAESLITG 64
QY	:: :
Db	196 FSEESI-----RDAMM--INAARKPVILGGVINAIPVERLAERQLPRT 241
QY	232 HALGGKQYIOPENPPFGMGLGGYACVQASNEADLLILGTPF----PYSDFLPKD 285
Db	242 MTLMAGMLPKAPLSLGMGMHGVFRSTNYLQDADLTLVIGARFDRAKGTEQFCPNA 301
QY	286 NVAQVINGANGIIGRRTVKG--IYGDVATIILPHKEKTDPSFLDRMLKHNKR- 341
Db	302 KIHVDIDRALGK---IKQPHVAQADVDPVLAQFLIPV-FAQPRRAHWLOVADREF 357
QY	342 --LSSVETVTHNVKHVPPIHPEVYASILNELA--DKDAVFTVDTGMCNVWHARY- 1 393
Db	394 ENPEGRDFDFVFSFRHGMANALPHATGAQSVDRNQVIAMCGGGGMLGIGELIVKLHQ 453
QY	405 NRPA--RQWLSSGGLGTMGFLPAATGAANPDRKVLCFSGDGSMMNIQMATSENQ 461
Db	454 IPLKAVVFNNSLGM--KLEMVVEGPEFGTDIEFVNFIAIANGRKRSPITRKKV 511
Db	462 LDVKITIMNNEARGLWHQQSLFVEQCVAATPGKINFMQIAEGFLETCDLNNEADPO 521
QY	512 EQLAELAYPGLVLTIVTDNAL--SIPPTITWQVMG 548
Db	522 ASLQEITINRPGPALIHRDAEERKVPMVFFGRANTEMVG 561
RESULT	10
ID	ILVBN_SP1PL
RT	STANDARD; PRT; 579 AA.
AC	P27868; 01-AUG-1992 (Rel. 23, Created)
DT	01-OCT-1996 (Rel. 34, Last annotation update)
DT	01-OCT-1996 (Rel. 34, Last annotation update)
DE	ACETOLACTATE SYNTHASE (EC 4.1.3.18) (ACETOHYDROXY-ACID SYNTHASE) (ALS)
RA	Milano A., de Rossi E., Zanaria E., Barblerato L., Ciferri O., Riccardi G.;
RT	"Molecular characterization of the genes encoding acetohydroxy acid synthase in the cyanobacterium <i>Spirulina platensis</i> .;"
RL	J. Gen. Microbiol. 138:1395-1408(1992).
CC	-I- CATALYTIC ACTIVITY: 2-ACETOLACTATE + CO(2) = 2 PYRUVATE.
CC	-I- COFACTOR: THIMINE PYrophosphate, AND MAGNESIUM ION.
CC	-I- PATHWAY: FIRST STEP IN VALINE AND ISOLEUCINE BIOSYNTHESIS.
CC	-I- SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.
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DR	EMBL; M75907; AA26595.1; -.
DR	PIR; B44857; B44857.
DR	HSSP; P06169; IYPD.
DR	INTERPRO; IPR00399; -.
DR	PFAM; PF00205; TPP_enzymes; 1..
DR	PROSITE; PS00187; TPP_ENZYMES; PARTIAL.
KW	BRANCHED-CHAIN AMINO ACID BIOSYNTHESIS; Flavoprotein; Lyase;
FT	ACT_SITE 60 61 BY SIMILARITY.
FT	NON_TER 579 579 NON_TER
SEQUENCE	579 AA; 63440 MW; BC94FEA728A7889A CRC64;

Query Match 17.3%; Score 517.5; DB 1; Length 579;
Best Local Similarity 27.8%; Pred. No. 1e-26; Mismatches 223; Indels 79; Gaps 19;
Matches 158; Conservative 108; -

QY 9 LIDITTLEAQVVRIGLVGDSLNPPIVD---AVRQSDEIWEHVWVRRNEEAAFARGAESLTG 64
|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 17 LIDSLRRIGVQHIGVPGGSNLPVYBIRREQAEIKHYLVRHEGAHAADGYARSTG 76
|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
QY 65 ELAVCAASCGPNTLHQGLUDSHRGAKVATASHIPSADGSTFQE----HPEI 118
|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 77 KVGVLCLATSGPATNLVTGLAYTAYLDSVPVLAITGQVPRSAUTDARQEIIDFGIMTPV 136
|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Qy 119 LFKECSGYCEMVNGGSGOGERILHATOSTMAGKGVSVVRCGDIKEADGCTYSNTIS 178
|||:|||:|||:|||:|||:|||:|||:|||:
Db 137 ---KHSYLVERPSELPRIVVEAFLHAMSGRGPVVL---DIPK-DVGNQADIVPVE 186
|||:|||:|||:|||:|||:|||:
Qy 179 SGT-----PVVFDPTEANALVEATNAKSVTLCGAG--VKNARAQVLELAERIKSP 229
|||:|||:|||:|||:|||:|||:|||:
Db 187 PGSVRRVGYRPTERGPRQINQALQLISEATKPLLVGGGIMAGAHAEELSEREQIP 246
|||:|||:|||:|||:
Qy 230 IGHALGCKQYIHHENPFEGVSGLUGYGACVDAAS--NEAALLLIGTDF----PYSD 280
|||:|||:|||:
Db 247 VSTSLMGKGDRDENHNEDLSLGIVGMCMHGTYANFAFMELDFVIAVGVRFDDRVACTGDQ 306
|||:|||:|||:
Qy 281 FLPKDNQVAQVDINGAHIGRRTVYKPYVTDGVMATIENILPHVKEKTDRLMLKAH-E 339
|||:|||:|||:
Db 307 FAHSKVIHIDIDPAEVGKNRSTDVPIVGDVROVGDML-----QRTY-----HWE 352
|||:|||:
Qy 340 RKLSSIVE--TYTHNEKHWIPI--HPEYVASTLN--ELADK--DAVFTVDTGNCNVW 388
|||:|||:
Db 353 RKLNRKPNRGTDLNQREPPLPTVPHPEDGSPQDGDWLSHQCPDAFFYTDVGQHOMW 412
|||:|||:
Qy 389 HARYIENPEGTRDVGSPHRGTMANALPHAQASVDRNRYVIAAMCGDGGLGMIGLELLT 448
|||:|||:
Db 413 AGQFVON-GPERRWMSSGGLGTMGYGLPAANGVKAVALPHDPTCISGDDGRQMNNQELGT 470
|||:|||:
Qy 449 VKLIQOLPLKAVVFNNSLGMVYKLEMVEGQPEFGDHEEV-----NFREIAAAGIK 500
|||:|||:
Db 471 IAQYGICGVKVTILLINGWLGWYR---QWQHMFYNDRYEATNLLEDGTPEFARLADVYLE 525
|||:|||:
Qy 501 SVRITDPKKVREQLABALAYPGPVLDI 528
|||:|||:
Db 526 AMVYRORKVYORRLPKALSHKGPMILDV 553
|||:|||:

RESULT 11
ILVG_ECOLI
ID ILVG_ECOLI STANDARD: PRT: 548 AA.
AC P00892; PT6749;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DE 1997 (Rel. 35, Last annotation update)
DE ACETOYLATE SYNTHASE ISOCYME II LARGE SUBUNIT (EC 4.1.3.18) (AHAS-II)
DE (ACETOHYDROXY-ACID SYNTHASE II LARGE SUBUNIT) (ALS-II).
GN ILVG.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
RN [1] SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RN STRAIN="K12";
RN MEDLINE="81174741; PubMed=3550695; "
RN Lawtner R.P., Wek R.C., Lopes J.M., Pereira R., Taillon B.E.,
RA Hatfield G.W.;
RT "The complete nucleotide sequence of the ilvgmE2 operon of
Escherichia coli K-12.";
RL Nucleic Acids Res. 15:2137-2155(1987).
RN [2] SEQUENCE FROM N.A.
RC STRAIN="K12 / MC1655; MEDLINE="92358234; PubMed=1379743;
RA Danielis D.L., Plunkett G. III, Burland V.D., Blattner F.R.,
RA INTERPRO; IPRO00399; -.

RT "Analysis of the Escherichia coli genome: DNA sequence of the region from 84.5 to 86.5 minutes.";
RT Science 257:771-778(1992).
RL [3]
RN
RP STRAIN=K12 / MUTANT ILV02096;
RX MEDLINE=81169435; PubMed=7015336;
RA Lawther R.P., Calhoun D.H., Adams C.W., Hauser C.A., Gray J.,
RA Hatfield G.W.;
RT "Molecular basis of valine resistance in Escherichia coli K-12.";
Proc. Natl. Acad. Sci. U.S.A. 78:922-925(1981).
RN [4]
RP SEQUENCE OF 1-402 FROM N.A.
RX STRAIN=K12;
RX MEDLINE=91138982; PubMed=1995430;
RA Coppola G., Huang F., Riley J., Cox J.L., Hantzopoulos P., Zhou L.-B.,
RA Calhoun D.H.;
RT "Sequence and transcriptional activity of the Escherichia coli K-12 chromosome region between rrnC and ilvgmE2.";
RL Gene 97:21-27(1991).
RN [5]
RP SEQUENCE OF 543-548 FROM N.A.
RX STRAIN=K12;
RA MIDDLE=85289113; PubMed=3897211;
RA Kuramitsu S., Ogawa T., Ogawa H., Kogamiyama H.;
RA "Branched-chain amino acid aminotransferase of Escherichia coli: nucleotide sequence of the ilvg gene and the deduced amino acid sequence.";
RA J. Biochem. 97:993-999(1985).
RN [6]
RP SEQUENCE OF 1-14 FROM N.A.
RX MIDDLE=80190145; PubMed=6154938;
RA Lawther R.P., Hatfield G.W.;
RT "Multivalent translational control of transcription termination at attenuator of ilvgEDA operon of Escherichia coli K-12.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:1862-1866(1980).
CC -- CATALYTIC ACTIVITY: 2-ACETOLACTATE + CO(2) = 2-PYRUVATE (THIS ENZYME ALSO CATALYZES FORMATION OF 2-ACETO-2-HYDROXYBUTANOATE).
CC -- COFACTOR: THIAMINE PYROPHOSPHATE, AND MAGNESIUM ION.
CC -- PATHWAY: FIRST STEP IN VALINE AND ISOLEUCINE BIOSYNTHESIS.
CC -- SUBUNIT: TETRAMER OF TWO LARGE AND TWO SMALL CHAINS.
CC -- MISCELLANEOUS: E. COLI CONTAINS GENES FOR 3 AHAS ISOCYMES: ILVN, ILVG AND ILVH. ONLY THE VAL-INHIBITABLE ILVN & ILVH ARE EXPRESSED. THE ILVG MUTATION, THE ILV02096 MUTATION (AN INSERTION OF 2 BP) CAUSES A FRAMESHIFT IN TRANSLATION, PERMITTING THE EXPRESSION OF THIS ISOZYME.
CC -- SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.
CC -----
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CC -----
DR EMBL; M10313; AAB59050.1;
DR EMBL; X00290; CAA2853.1; -
DR EMBL; M87049; AAB6751.1; ALT_SEQ.
DR EMBL; AE000453; AAC77488.1; ALT_SEQ.
DR EMBL; M32253; AAA24021.1; -
DR EMBL; M37337; AAA4608.1; -
DR EMBL; X02413; CAA26260.1; -
DR EMBL; V00289; CAA2356.1; -
DR EMBL; M8570; YEC.
DR PIR; JQ0875; JQ0875.
DR PIR; S30665; S30665.
DR PIR; S30665; S30666.
DR HSSP; P06169; YPD.
DR ECOGENE; EG1048; ILVG.
DR INTERPRO; IPRO00399; -.

DT 01-OCT-2000 (Rel. 40; Last annotation update)
DE ACETOLACTATE SYNTHASE PRECURSOR (EC 4.1.3.18) (ACETOHYDROXY-ACID
SYNTHASE) (ALS).
GN CSR 1..2.
OS Arabidopsis thaliana (Mouse-ear cress); Tracheophyta; Spermatophyta;
Eukaryota; Viridiplantae; Embryophyta; Brassicales; Brassicaceae; Arabidopsis.
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
RN [1]
RP SEQUENCE FROM N A.
RC STRAIN-CV. COLUMBIA;
RX MEDLINE=90245681; PubMed=2336405;
RA Sathasivan K., Haughn G.W., Murai N.;
RT "Nucleotide sequence of a mutant acetolactate synthase gene from an
imidazolinone-resistant Arabidopsis thaliana var. Columbia.";
RL Nucleic Acids Res. 18:2188-2188(1990).
RN [2]
RP VARIANT GH30.
RC STRAIN-CV. COLUMBIA;
RA Sathasivan K., Haughn G.W., Murai N.;
RT "Molecular basis of imidazolinone herbicide resistance in Arabidopsis
thaliana var. Columbia.";
RL Plant Physiol. 97:104-105(1991).
CC -!- CATALYTIC ACTIVITY: 2-ACETOLACTATE + CO(2) = 2-PYRUVATE (THIS
ENZYME ALSO CATALYZES FORMATION OF 2-ACETO-2-HYDROXY-BUTANOATE).
CC -!- COFACTOR: THIAMINE PYROPHOSPHATE, AND MAGNESIUM ION.
CC -!- PATHWAY: FIRST STEP IN VALINE AND ISOLEUCINE BIOSYNTHESIS.
CC -!- MISCELLANEOUS: ACETOLACTATE SYNTHASE IS THE TARGET ENZYME FOR
SULFONYLUREA AND IMIDAZOLINONE HERBICIDES. MUTANT GH 90 IS
RESISTANT TO IMIDAZOLINONE HERBICIDES AND MUTANT GH 50 TO
SULFONYLUREA.
CC -!- BIOTECHNOLOGY: INTRODUCED BY GENETIC MANIPULATION AND EXPRESSED IN
SULFONYLUREA RESISTANT FLAX BY THE UNIVERSITY OF SASKATCHEWAN.
CC -!- SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.

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CC EMBL: X51514; CNA35887.1; -.
DR PIR; S09502; YCNU.
DR HSSP; P06169; IYPD.
DR INTERPRO; IPR000399; -.
DR PFAM; PF00205; TPP_enzymes; 1.
DR PROSITE; PS00187; TPP_ENZMES; 1.
KW Branched-chain amino acid biosynthesis; Flavoprotein; Magnesium;
Thiamine pyrophosphate; Herbicide resistance; Transient peptide;
Lyase; Chloroplast; Genetically modified food.
FT TRANSIT 1 97 CHLOROPLAST.
FT CHAIN 98 670 ACETOLACTATE SYNTHASE.
FT ACT_SITE 144 144 BY SIMILARITY.
FT VARIANT 197 197 P -> S (IN MUTANT GH 50).
FT VARIANT 653 653 S -> N (IN MUTANT GH 90).
FT SEQUENCE 670 AA; 72585 MW; DA697A8DD155F160 CRC64;

Query Match 16.5%; Score 493; DB 1; Length 670;
Best Local Similarity 27.5%; Pred. No. 5e-25; Gaps 14;
Matches 158; Conservative 97; Mismatches 259; Indels 60; Gaps 14;

Qy 6 AEQLDITLEQCGKRYIGLVLGDSLNPIVDV-RQSDIEWMHVRBEAAAGARSLLTG 64
Db 100 ADLVLVERLEROGLVETWVPGASMEIHOALTSSRSIRNVLPRHOGGVFAEGYARSSG 159
Qy 65 ELAVCAASCIGPGNHLIQGLYDHRNGAKVIALAISHPSAQIGSTFFQETHPELFKECS 124
Db 160 KPGCIATSGCGATNLVSLGLADLLSPVLAITQVPRMIGTOAQESPIVEVTSIT 219
Qy 125 GYCEMVNGGEOGERILUHIAOSTMAGK-GVSVWVPGDIKEDASDGTYNSTLSSGTPV 183

Db 220 KNYLMDVEDIPRIEEAFFLFLATSGRGPVPLVDVKD1-QQQLAIPNWEQAMRLPGYMS 278
Qy 184 VEPDPTEAAL---VERINAKSVTJFCGAGVKAARAQVLEBLAEKIKSPICHALGGQYI 240
CC 279 RMPKPPDHSIIEQVIRLSEKKPVLYVGCGCLNSDELREFVELTGIPVASTLKGYS 338
Db 339 PCDDELSLHMLGMHGTVYAVANVAEVHSDLLAFLGVREDRIVKLEAFASRAKIVHIDS 398
Qy 295 AHGRRRTVVKPVTGDAATTENILPHVKEKTDRLM--KAERKIKSSVWEYTHN 352
Db 399 AEIGKNKTPPHVSVCGDVKLALQG-----MNKVLLENRAEELKLDGFVWRNELN 445
Qy 353 VEKH-----VPIHPENVVASIUNELADKDAVTFVTGMCNUHARVYENPECTRD 402
Db 446 VOKQKEPLSKTFKFGEAIPPKQAIKVDELTGKAIISTGQHOMMAQFY-NYKPRP 504
Qy 403 VGSFRHGTMANALPHAIGAQSVDRNRQVIMAGCGDGGGMLGELVTKLHQPLKAVEN 462
Db 505 LSSGGLGAMGPGCLPAAGASVANPDAIWIDGDSFIMVQELATIREVNLPVKVLLN 564
Qy 463 NSSLGWMVLEMVE-----GQPRTGTDIEEV--NFAEAAAGKSYRITDP 507
Db 565 NOHLGMY--NMOWEDRFYKANRAHTFLGDPP--AQEDEFPNMLLFAACGIPAARTVK 618
Qy 508 KVREQLAELAYPGVLDIVDPNALSIPTI 541
GN SPXB
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
RN [1]
RP SEQUENCE FROM N A.
RC STRAIN-6X;
RX MEDLINE=961717859; PubMed=8820650;
RA Spellerberg, B., Cundell D.R., Sandros J., Pearce B.J.,
RA Idanpean-Hekkila I., Rosenow C., Masure H.R.,
RT "Pyruvate oxidase, as a determinant of virulence in Streptococcus
pneumoniae".
RL Mol. Microbiol. 19:803-813(1996).
CC -!- FUNCTION: IMPORTANT FOR THE AEROBIC GROWTH. DECARBOXYLATES
PYRUVATE IN FOUR STEPS. THE ENERGY RELEASED IS PARTIALLY STORED
IN ACETYL PHOSPHATE (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: PYRUVATE + ORTHOPHOSPHATE + O(2) + H(2)O -
CC -!- ACETYL PHOSPHATE + CO(2) + H(2)O(2).
CC -!- COFACTOR: THIAMINE PYROPHOSPHATE, FAD AND MAGNESIUM ION (BY
SIMILARITY).
CC -!- SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.

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CC DR L39074; KAB40976.1; -.
DR PFAM; PF00205; TPP_enzymes; 1.

DR	PROSITE; PS00187; TPP_ENYMES; 1.	Score 492; DB 1; Length 591;	RL	Mol. Gen. Genet. 229:31-40(1991).
KW	Oxidoreductase; Flavoprotein; FAD; Thiamine Pyrophosphate; Magnesium.	Best Local Similarity 16.5%; Score 492; DB 1; Length 591;	CC	-I- CATALYTIC ACTIVITY: 2-ACETO-LACTATE + CO(2) = 2-PYRUVATE (THIS
FT	DOMAIN 1 188	Pred. No. 4.9e-25;	CC	ENZYME ALSO CATALYZES FORMATION OF 2-AETO-2-HYDROXY-BUTANOATE).
FT	DOMAIN 189 336	Mismatches 146; Conservative 110; Indels 50; Gaps 13;	CC	-I- COFACTOR: THIAMINE PYROPHOSPHATE, AND MAGNESIUM ION.
FT	DOMAIN 337 591	Matches 146; Mismatches 230; Indels 50; Gaps 13;	CC	-I- PATHWAY: FIRST STEP IN VALINE AND ISOLEUCINE BIOSYNTHESIS.
FT	ACT SITE 53 53	Score 492; DB 1; Length 591;	CC	-I- MISCELLANEOUS: ACETO-LACTATE SYNTHASE IS THE TARGET ENZYME FOR
FT	METAL 441 441	BY SIMILARITY).	CC	SULFONYLUREA AND IMIDAZOLINONE HERBICIDES.
FT	METAL 468 468	MAGNETIUM (BY SIMILARITY).	CC	-I- SIMILARITY: WITH OTHER ENYMES WHICH REQUIRE TPP.
FT	METAL 470 470	MAGNESIUM (BY SIMILARITY).	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
SQ	SEQUENCE 591 AA; 65128 MW; C02462214138635F CRC64;	between the European Bioinformatics Institute and the EMBL outstation	CC	use by non-profit institutions as long as its content is in no way
Query	9 LIDTLDEAQVKYKRIYGLVGDSINPPIVDAVRQ-SDDIWVHVRNEEAAFAAGAESLTGELA 67	modified and this statement is not removed. Usage by and for commercial	CC	entities requires a license agreement. (See http://www.isb-sib.ch/announce/)
Db	12 MLNVLKWTWGVDTIGIPSCVLSSMADAKDKTDREFLQRHEETGALAAVMQARGGSIG 71	or send an email to license@isb-sib.ch).	CC	CC
Qy	68 VCAASCGPGNHLIOGLYDLSNRNGAKVLAIAASHIPTSAQIGSTFFROETHPEITLPKBCSGYC 127	DR	EMBL: Z11524; CA77613.1; -.	
Db	72 VAVGGGGPAGATHLINGVYDAAMNDNPFLATLGSRVNELNMADFQELNQNPMYNGIAVN 131	DR	PTR: S17691; S17691.	
Qy	128 EMVNGSGEQEGETILHHIAQSTMAGKEVSVVWIPGDIAKEDA---GDGIVSNPSNTSGT 181	DR	HSP: P06169; IYPD.	
Db	132 KRVAYAEOLPKVWDEACRAATSKPGAVVEIPVNFQFOETDENSYYGGSYERSFTA-- 188	DR	INTERPRO: IPR00399; -.	
Qy	182 PVFPDPTEAAVALLVEINNAKSVALTFCAGYKVARAQVLEAKKSPIGHALGSQKQVIO 241	DR	PFAM: PF00205; TPP_enzymes; 1.	
Db	189 PAL--NEVELDKAPELLNNAERPVTIVAGFGGVKAEGEVITELSRKIKAPI--ITTCGNFEEA 244	DR	PROSITE; PS00187; TPP_ENYMES; 1.	
Qy	242 HENPFEGVMSG--LLGYGACYDASNEADLJLGLDFPVSD---FLPKDNVAQYDING 294	DR	Thiamine Pyrophosphate; Herbicide resistance; Transit peptide;	
Db	245 FEWNYE-GLTGSAYRVGWPANEVWEADTVLFGLSNFAEVYEAFKNTEKFIQVDIP 303	DR	Lyase; Chloroplast; Multigene family.	
Qy	295 AHIGRRRTVVKYPTVGVAAATIENILPHVKE-----KTIDSFLDRMLKAHERKLK 343	DR	TRANSIT 1 82 CHLOROPLAST (BY SIMILARITY).	
Db	304 YKLGRKHADASILGDAQQAALKALDKVNPNVESTPWANRKNQNWDRYMNKL-EGKTE 362	DR	CHAIN 83 655 ACETO-LACTATE SYNTHASE I.	
Qy	344 SVETVTHNVEKHPVHPEVYASILNEALDKDAVFTVDTGMCNWNHARYE-NPEGTRDF 402	FT	ACT_SITE 129 129 BY SIMILARITY.	
Db	363 GELQLY-----QVYNTAKHADDAITYSLDVGSTHTSTRHLHMPTRNM-W 407	FT	SEQUENCE 655 AA; 71288 MW; 1BAD7D7A0DA91A CRC64;	
Qy	403 VGSFRHGTMANALPHAIAGAQSVDRNQVIAMCGDGGMIGLIGELITVQLHQPLPKAVFN 462	Query	Query Match 16.1%; Score 480; DB 1; Length 655;	
Db	408 RTSPLEATMGIALPGGIAAKDTPDRQWVNIMGDGAFMQYDPVITNQYDLPVINLVFS 467	Best Local Similarity 26.3%; Pred. No. 3.5e-24; Matches 149; Conservative 104; Mismatches 269; Indels 44; Gaps 12;		
Qy	463 NSSLGAVKLEMIVVEGQPEFGIDHEEVNFALAAAGIKSVRITDPKVREQLAEL 518	Db	AEQIDLTLEQOGVKYKLVGLVGDSINPPIVDAVRQ-ROSDIEWHVRNEEAAFAAGAESLTG 64	
Db	468 NAEYGFIIKNEYDTNKHFLGVDFTNADYGRKIAEQAVGFTVDRIEDIDAWAVEA 523	Qy	6 ADILVEALERQGVETWFAPFGGASMEIHQALTRSTSIRNLWPLRHEQGVFAEGYARSSG 144	
RESULT	15	Db	85 ELAVCAASCGPGNTILIQLYDLSNRNGAKVLAIAASHIPTSAQIGSTFFROETHPEITLPKCS 124	
ID	ILV1_BRANA	Qy	145 KPGICLATSPPGATNIUVSGLADAMLDSPVLPVATGQVPRRMIGTDAFOETPTVETRSIT 204	
ID	ILV1_BRANA STANDARD; PRT; 655 AA.	Db	125 GYCEMWNGGQGERILHHAQSTMAGK-GWSVWVIPGDIAKEDAGDTYNSNTISSGFV 183	
Qy	P27818; 01-AUG-1992 (Rel. 23, Last sequence update)	Db	205 KHNLYLVDVDPDIPRIVQEARFLATSGRPGVLPVQPKDI-QQQLAIPNWMDQPMPLPGMS 263	
DT	01-AUG-1992 (Rel. 23, Last sequence update)	Qy	184 VFPDPTEAAVALLVEINNAKSVALTFCAGYKVARAQVLEAKKSPIGHALGSQKQVIO 240	
DT	01-OCT-1996 (Rel. 34, Last annotation update)	Db	264 RLQPQPPEVSQDQVTLRILSESKRVPDQVYLVGGGLSNSSEELGRFVELTGIPVASTIMGLSY 323	
DE	ACETO-LACTATE SYNTHASE I PRECURSOR (EC 4.1.3.18) (ACETOHYDROXY-ACID SYNTHASE I) (ALS I).	Qy	241 QHENPFEGVMSGLGYGACYDASNEADLJLGLDF----PYSDELKKDNVAQYDING 294	
OS	Brassica napus (Rape).	Db	324 PCNDELSLOMLGMGHVYVANAVEHSDLLLAFGVFDRTVKGLEAFASRARKVHIDDS 383	
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.	Qy	295 AHIGRRRTVVKYPTVGVAAATIENILPHVKE-----KTIDSFLDRMLKAHERKLV 349	
RN	[1] SEQUENCE FROM N A.	Db	384 AEIGKKNTPHYSVCQDVKLQGMKVLENRAEELKUDGEGWWRSELQDQQKFELSEKF 443	
RP	SEQUENCE FROM N A.	Qy	350 THNVEKHPVHPEVYASILNEALDKDAVFTVDTGMCNWNHARYE-NPEGTRDFVGSFRG 409	
RC	STRAIN=CV_TOBAS; MEDLINE=91-75448; PubMed=1896019;	Db	444 GE----AIPPOVATQILDDELTEKGAIISTGVQHOMMAQFYKRYK PRQWLSSGLG 496	
RX	Rutledge R. G., Ouellet T., Hattori J., Miki B. L.; Molecular characterization and genetic origin of the Brassica napus acetoxyhydroxyacid synthase multigene family.;	Qy	410 TMANALPHAIAGAQSVDRNQVIAMCGDGGMIGLIGELITVQLHQPLPKAVFVNNSLGV 469	
RT		Db	497 AMGFLGPAIGASVANPDTAVVIDDGDSFTMNVQELATRIVENLIPVKILLNNOHGMV 556	
RT		Qy	470 KLEMVLVEQDF----GIDHE---VFAEIAAAAGIKSVRITDPKKVREQIA 515	
RT		Db	557 ----MOWEREFYKANRAHTYLGDPARENENEPNMLQFAGCIPAARVYTKKEELRAIQ 611	

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